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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/380,447	09/01/1999	Sachdev S. Sidhu	11669.141USWO ✓	2633

23552 7590 08/30/2007
MERCHANT & GOULD PC
P.O. BOX 2903
MINNEAPOLIS, MN 55402-0903

*BRD
KMK

EXAMINER

STEELE, AMBER D

ART UNIT	PAPER NUMBER
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1639

MAIL DATE	DELIVERY MODE
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08/30/2007

PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Seq Resp 1: 09/30/2007
Seq Resp 3/PTA: 11/30/2007
Seq Resp start: 02/29/2008
dv

**UNITED STATES DEPARTMENT OF COMMERCE****U.S. Patent and Trademark Office**

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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09380447	9/1/1999	SIDHU ET AL.	11669.141USWO

MERCHANT & GOULD PC
P.O. BOX 2903
MINNEAPOLIS, MN 55402-0903

EXAMINER

Amber D.. Steele

ART UNIT**PAPER**

1639

20070821

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

1)The present application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821 (a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825. The sequence listing has various errors as indicated in the attached Raw Sequence Listing and error report.

2)Applicant is given ONE MONTH from the date of this letter within which to comply with the Sequence Rules, 37 CFR 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In NO case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

3)Any inquiry concerning this communication or earlier communications from the examiner should be directed to Amber D. Steele whose telephone number is 571-272-5538. The examiner can normally be reached Monday through Friday 9:00AM-5:00PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Doug Schultz can be reached at 571-272-0763. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

ADS
August 21, 2007

MARK L. SHIBUYA
PRIMARY EXAMINER

Notice to Comply	Application No. 09/380,447	Applicant(s) S IDHU ET AL.	
	Examiner Steele, A. D.	Art Unit 1639	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set in the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: see attached PTO-90C.

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the application.**
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-2510

For CRF Submission Help, call (571) 272-2501/2583.

PatentIn Software Program Support

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PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Jul 30 14:06:26 EDT 2007

=====

Reviewer Comments:

<150> US 60/134,870

<151> 1999 05 19

<150> US 60/133,296

<151> 1999 05 10

<150> US 60/103,514

<151> 1998 10 08

<150> US 60/094,291

<151> 1998 07 27

<150> PCT/USUS99/16596

<151> 1999 07 22

The above non-ASCII characters ("squares") between dates appear
throughout the submitted sequence listing file; they also appear in
<222> responses which indicate locations within the sequence. Please
replace them with hyphens.

<400> 293

His His His His

1

69

Please remove the above "69" appearing at the end of the submitted file.

Application No: 09380447

Version No: 3.0

Input Set:

Output Set:

Started: 2007-07-19 18:29:54.051

Finished: 2007-07-19 18:31:26.799

Elapsed: 0 hr(s) 1 min(s) 32 sec(s) 748 ms

Total Warnings: 284

Total Errors: 366

No. of SeqIDs Defined: 292

Actual SeqID Count: 293

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <151>
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <151>
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E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <151>
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <151>
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 341	'Xaa' position not defined SEQID (1) POS (12)
E 341	'Xaa' position not defined SEQID (1) POS (13)
E 341	'Xaa' position not defined SEQID (1) POS (14)
E 341	'Xaa' position not defined SEQID (1) POS (15)
E 341	'Xaa' position not defined SEQID (1) POS (16)
E 341	'Xaa' position not defined SEQID (1) POS (17)
E 341	'Xaa' position not defined SEQID (1) POS (18)
E 341	'Xaa' position not defined SEQID (1) POS (19)
E 341	'Xaa' position not defined SEQID (1) POS (20)
E 341	'Xaa' position not defined SEQID (1) POS (21)
E 341	'Xaa' position not defined SEQID (1) POS (22)
E 341	'Xaa' position not defined SEQID (1) POS (23)
E 341	'Xaa' position not defined SEQID (1) POS (24)

Input Set:

Output Set:

Started: 2007-07-19 18:29:54.051
Finished: 2007-07-19 18:31:26.799
Elapsed: 0 hr(s) 1 min(s) 32 sec(s) 748 ms
Total Warnings: 284
Total Errors: 366
No. of SeqIDs Defined: 292
Actual SeqID Count: 293

Error code	Error Description
E 341	'Xaa' position not defined SEQID (1) POS (25)
E 341	'Xaa' position not defined SEQID (1) POS (26)
E 341	'Xaa' position not defined SEQID (1) POS (27)
E 341	'Xaa' position not defined SEQID (1) POS (28)
E 341	'Xaa' position not defined SEQID (1) POS (29)
E 341	'Xaa' position not defined SEQID (1) POS (30)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)

Input Set:

Output Set:

Started: 2007-07-19 18:29:54.051
Finished: 2007-07-19 18:31:26.799
Elapsed: 0 hr(s) 1 min(s) 32 sec(s) 748 ms
Total Warnings: 284
Total Errors: 366
No. of SeqIDs Defined: 292
Actual SeqID Count: 293

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
E 342	'n' position not defined found at POS: 20 SEQID(21)
E 342	'n' position not defined found at POS: 22 SEQID(21)
E 342	'n' position not defined found at POS: 26 SEQID(21)
E 342	'n' position not defined found at POS: 28 SEQID(21)
E 342	'n' position not defined found at POS: 31 SEQID(21)
E 342	'n' position not defined found at POS: 34 SEQID(21)
E 342	'n' position not defined found at POS: 38 SEQID(21)
E 342	'n' position not defined found at POS: 41 SEQID(21)
E 342	'n' position not defined found at POS: 44 SEQID(21)
E 342	'n' position not defined found at POS: 47 SEQID(21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
E 342	'n' position not defined found at POS: 19 SEQID(22)
E 342	'n' position not defined found at POS: 22 SEQID(22)
E 342	'n' position not defined found at POS: 26 SEQID(22)
E 342	'n' position not defined found at POS: 28 SEQID(22)
E 342	'n' position not defined found at POS: 31 SEQID(22)
E 342	'n' position not defined found at POS: 35 SEQID(22)
E 342	'n' position not defined found at POS: 38 SEQID(22)

Input Set:

Output Set:

Started: 2007-07-19 18:29:54.051
Finished: 2007-07-19 18:31:26.799
Elapsed: 0 hr(s) 1 min(s) 32 sec(s) 748 ms
Total Warnings: 284
Total Errors: 366
No. of SeqIDs Defined: 292
Actual SeqID Count: 293

Error code	Error Description
E 342	'n' position not defined found at POS: 41 SEQID(22)
E 342	'n' position not defined found at POS: 44 SEQID(22)
E 342	'n' position not defined found at POS: 46 SEQID(22) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (56)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (293)
E 252	Calc# of Seq. differs from actual; 292 seqIds defined; count=293

Sequence Listing

<110> Sidhu, Sachdev S.
Weiss, Gregory A.
Wells, James A.

<120> TRANSFORMATION EFFICIENCY IN PHAGE DISPLAY THROUGH MODIFICATION OF A
COAT PROTEIN

<130> 11669.141USWO

<140> 09380447

<141> 1999-09-01

<150> US 09/380,447

<151> 1999 09 01

<150> US 60/134,870

<151> 1999 05 19

<150> US 60/133,296

<151> 1999 05 10

<150> US 60/103,514

<151> 1998 10 08

<150> US 60/094,291

<151> 1998 07 27

<150> PCT/USUS99/16596

<151> 1999 07 22

<160> 292

<210> 1

<211> 50

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic coat protein

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<221> unsure

<222> 12 30

<223> unknown amino acid

<400> 1

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				20					25					30

Glu	Thr	Ala	Ser	Ala	Gln	Leu	Ser	Asn	Phe	Ala	Ala	Lys	Ala	Pro
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Asp Asp Gly Glu Ala
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<211> 50

<212> PRT

<213> M13 phage

<220>

<221> M13 phage

<222> 1 50

<223> coat protein VIII

<400> 2

Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asn Ser Leu Gln
1 5 10 15

Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
20 25 30

Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
35 40 45

Thr Ser Lys Ala Ser
50

<210> 3

<211> 50

<212> PRT

<213> f1 phage

<220>

<221> f1 phage

<222> 1 50

<223> coat protein VIII

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Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asp Ser Leu Gln
1 5 10 15

Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
20 25 30

Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
35 40 45

Thr Ser Lys Ala Ser
50

<210> 4

<211> 50

<212> PRT

<213> fd phage

<220>

<221> fd phage

<222> 1 50

<223> coat protein VIII

<400> 4

Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asp Ser Leu Gln
1 5 10 15

Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
20 25 30

Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
35 40 45

Thr Ser Lys Ala Ser
50

<210> 5

<211> 50

<212> PRT

<213> Zj 2 phage

<220>

<221> Zj 2 phage

<222> 1 50

<223> coat protein VIII

<400> 5

Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asp Ser Leu Gln
1 5 10 15

Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
20 25 30

Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
35 40 45

Ala Ser Lys Ala Ser
50

<210> 6

<211> 50

<212> PRT

<213> Ifl phage

<220>

<221> Ifl phage

<222> 1 50

<223> coat protein VIII

<400> 6

Asp Asp Ala Thr Ser Gln Ala Lys Ala Ala Phe Asp Ser Leu Thr
1 5 10 15

Ala Gln Ala Thr Glu Met Ser Gly Tyr Ala Trp Ala Leu Val Val
20 25 30

Leu Val Val Gly Ala Thr Val Gly Ile Lys Leu Phe Lys Lys Phe
35 40 45

Val Ser Arg Ala Ser
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<210> 7
<211> 50
<212> PRT
<213> I2 2 phage

<220>
<221> I2 2 phage
<222> 1 50
<223> coat protein VIII

<400> 7
Ser Thr Ala Thr Ser Tyr Ala Thr Glu Ala Met Asn Ser Leu Lys
1 5 10 15

Thr Gln Ala Thr Asp Leu Ile Asp Gln Thr Trp Pro Val Val Thr
20 25 30

Ser Val Ala Val Ala Gly Leu Ala Ile Arg Leu Phe Lys Lys Phe
35 40 45

Ser Ser Lys Ala Val
50

<210> 8
<211> 50
<212> PRT
<213> Ike phage

<220>
<221> Ike phage
<222> 1 50
<223> coat protein VIII

<400> 8
Asn Ala Ala Thr Asn Tyr Ala Thr Glu Ala Met Asp Ser Leu Lys
1 5 10 15

Thr Gln Ala Ile Asp Leu Ile Ser Gln Thr Trp Pro Val Val Thr
20 25 30

Thr Val Val Val Ala Gly Leu Val Ile Arg Leu Phe Lys Lys Phe
35 40 45

Ser Ser Lys Ala Val
50

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<223> oligonucleotide primer

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<210> 10

<211> 35

<212> DNA

<213> Artificial sequence

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<223> oligonucleotide primer

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<210> 11

<211> 56

<212> DNA

<213> Artificial sequence

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<223> oligonucleotide primer

<400> 11

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atcgtc 56

<210> 12

<211> 34

<212> DNA

<213> Artificial sequence

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<223> oligonucleotide primer

<400> 12

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<211> 61

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aggtgtcgtg g 61

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<210> 15
<211> 46
<212> DNA
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<210> 17
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<220>

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<400> 17
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<210> 18
<211> 42
<212> DNA
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<220>

<223> mutagenic oligonucleotide

<400> 18
caagcctcag cgaccgaatg atgaggttat gcgtgggcga tg 42

<210> 19
<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<400> 19

cgctgggcga tgggtgtttg atgagtcggc gcaactatcg gt 42

<210> 20

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<400> 20

gcaactatcg gtatcaagtg atgaaagaaa ttcacctcga aa 42

<210> 21

<211> 66

<212> DNA

<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<220>

<221> unsure

<222> 20, 22, 26, 28, 31, 34, 38, 41, 44, 47

<223> unknown base

<400> 21

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taactccctg caagcc 66

<210> 22

<211> 66

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<223> mutagenic oligonucleotide

<220>

<221> unsure

<222> 19, 22, 26, 28, 31, 35, 38, 41, 44, 46

<223> unknown base

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tatcggttat gcgtgg 66

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 <221> unsure
 <222> 19, 22, 25, 28, 31, 35, 38, 41, 44, 47
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 tcattgtcgg cgcaactatc 70

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 <211> 66
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> mutagenic oligonucleotide

 <220>
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 <222> 19, 22, 25, 28, 31, 34, 37 38, 40 41, 43 44
 <223> unknown base

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 gtttaagaaa ttcacc 66

 <210> 25
 <211> 72
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> mutagenic oligonucleotide

 <220>
 <221> unsure
 <222> 19 20, 22 23, 31 32, 34 35, 37 38, 43 44, 46 47
 <223> unknown base

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 ataaaccgat acaattaaag gc 72

 <210> 26
 <211> 66
 <212> DNA

<213> Artificial sequence

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<223> mutagenic oligonucleotide

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tatcggttat gcgtgg 66

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<211> 36

<212> DNA

<213> Artificial sequence

<220>

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<210> 28

<211> 36

<212> DNA

<213> Artificial sequence

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<223> mutagenic oligonucleotide

<400> 28

ttcaggaagg acatggctaa ggtcgagaca ttcttg 36

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<211> 75

<212> DNA

<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<400> 29

aactacgggc tgctcgcttg cttcaggaag gacatggaca aggtcgagac 50

attcctggct atcgtgcagt gccgc 75

<210> 30

<211> 57

<212> DNA

<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<400> 30

ttcaggaagg acatggacgc tgtcgagaca ttctggcta tcgtccagtg 50

ccgctct 57

<210> 31

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<400> 31

ggtggaggat ccgggagctg atgagccgag ggtgacgac cc 42

<210> 32

<211> 46

<212> DNA

<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<400> 32

caccaagggtg gtctagagct aataataagc cgagggtgac gatccc 46

<210> 33

<211> 50

<212> PRT

<213> Artificial sequence

<220>

<223> P12 1 variant

<400> 33

Met	Ser	Lys	Ser	Thr	Phe	Lys	Lys	Phe	Leu	Lys	Val	Phe	Val	Phe
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				20				25					30	

Tyr	Met	Leu	Leu	Val	Glu	Ala	Ser	Pro	Trp	Ala	Ala	Lys	Ala	Pro
				35				40					45	

Asp	Asp	Gly	Glu	Ala
				50

<210> 34

<211> 93

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide linker library

<400> 34

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